

RAW SEQUENCE LISTING

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Application Serial Number: 10/593,425
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/593,425

TIME: 14:48:25

Input Set : E:\13744- 21 US Sequence Listing.txt

Output Set: N:\CRF4\10102006\J593425.raw

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3 <110> APPLICANT: Feesche, Jorg
4     Meinhardt, Friedhelm
5     Nahrstedt, Hannes
6     Waldeck, Jens
7     Groene, Mark
8     Eichstadt, Renee
10 <120> TITLE OF INVENTION: Factor RecA From Bacillus Licheniformis and RecA-inactivated
11     Safety Stems Used for Biotechnological Production
13 <130> FILE REFERENCE: H 06291 (13744*21)
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/593,425
C--> 15 <141> CURRENT FILING DATE: 2006-09-19
15 <150> PRIOR APPLICATION NUMBER: PCT/EP05/001543
16 <151> PRIOR FILING DATE: 2005-02-16
18 <150> PRIOR APPLICATION NUMBER: DE 10 2004 013 988.1
19 <151> PRIOR FILING DATE: 2004-03-19
21 <160> NUMBER OF SEQ ID NOS: 32
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1047
27 <212> TYPE: DNA
28 <213> ORGANISM: Bacillus licheniformis DSM 13
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1047)
35 <220> FEATURE:
36 <221> NAME/KEY: gene
37 <222> LOCATION: (1)..(1047)
38 <223> OTHER INFORMATION: recA
41 <400> SEQUENCE: 1
42 atg agt gat cgt cag gca gcc tta gat atg gcg ctt aaa caa ata gaa      48
43 Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln Ile Glu
44 1             5             10             15
46 aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa act gaa      96
47 Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu
48             20             25             30
50 acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat gcg gct      144
51 Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
52             35             40             45
54 ctt gga gtg ggc gga tac ccg cgc ggc cgg att att gaa gta tac ggg      192
55 Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
56             50             55             60
58 cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att gcc gaa      240
59 Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu

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60	65					70				75				80					
62	gtt	cag	cag	cag	ggc	gga	caa	gcg	gcg	ttc	atc	gac	gcc	gac	acc	gcg			288
63	Val	Gln	Gln	Gln	Gly	Gly	Gln	Ala	Ala	Phe	Ile	Asp	Ala	Asp	Thr	Ala			
64					85					90				95					
66	ctt	gat	ccc	gtc	tat	gca	caa	aag	ctg	ggc	gtc	aac	att	gat	gag	ctt			336
67	Leu	Asp	Pro	Val	Tyr	Ala	Gln	Lys	Leu	Gly	Val	Asn	Ile	Asp	Glu	Leu			
68				100					105					110					
70	ttg	ctg	tca	cag	cct	gat	acg	ggc	gag	cag	gcg	ctc	gaa	atc	gct	gaa			384
71	Leu	Leu	Ser	Gln	Pro	Asp	Thr	Gly	Glu	Gln	Ala	Leu	Glu	Ile	Ala	Glu			
72				115					120					125					
74	gcc	ctt	gtc	aga	agc	gga	gcg	gtg	gat	atc	gtt	gtc	atc	gac	tct	gta			432
75	Ala	Leu	Val	Arg	Ser	Gly	Ala	Val	Asp	Ile	Val	Val	Ile	Asp	Ser	Val			
76		130				135						140							
78	gca	gcg	ctt	gtg	ccg	aaa	gct	gaa	atc	gaa	gga	gat	atg	ggg	gat	tcc			480
79	Ala	Ala	Leu	Val	Pro	Lys	Ala	Glu	Ile	Glu	Gly	Asp	Met	Gly	Asp	Ser			
80	145				150					155				160					
82	cac	gtc	ggt	ttg	cag	gcc	aga	ctg	atg	tct	cag	gcg	ctt	cgc	aag	ctt			528
83	His	Val	Gly	Leu	Gln	Ala	Arg	Leu	Met	Ser	Gln	Ala	Leu	Arg	Lys	Leu			
84				165					170					175					
86	tcc	gga	gcg	atc	aat	aaa	tcg	aag	acc	atc	gcg	atc	ttt	atc	aac	cag			576
87	Ser	Gly	Ala	Ile	Asn	Lys	Ser	Lys	Thr	Ile	Ala	Ile	Phe	Ile	Asn	Gln			
88				180					185					190					
90	att	cgt	gaa	aaa	gtc	ggt	gtc	atg	ttt	gga	aat	cct	gag	acg	acg	cca			624
91	Ile	Arg	Glu	Lys	Val	Gly	Val	Met	Phe	Gly	Asn	Pro	Glu	Thr	Thr	Pro			
92				195					200					205					
94	ggc	gga	aga	gcg	ctg	aaa	ttc	tac	tct	tct	gtc	cgc	ctt	gaa	gtg	cgc			672
95	Gly	Gly	Arg	Ala	Leu	Lys	Phe	Tyr	Ser	Ser	Val	Arg	Leu	Glu	Val	Arg			
96		210				215						220							
98	cgc	gca	gag	cag	ctg	aaa	caa	ggc	aac	gac	gtc	atg	ggg	aac	aag	acg			720
99	Arg	Ala	Glu	Gln	Leu	Lys	Gln	Gly	Asn	Asp	Val	Met	Gly	Asn	Lys	Thr			
100	225				230					235				240					
102	aaa	atc	aaa	gtc	gtg	aaa	aac	aaa	gtg	gca	cct	cca	ttc	cgg	aca	gcc			768
103	Lys	Ile	Lys	Val	Val	Lys	Asn	Lys	Val	Ala	Pro	Pro	Phe	Arg	Thr	Ala			
104				245						250				255					
106	gaa	gtg	gac	att	atg	tac	ggg	gaa	gga	att	tca	aaa	gaa	ggg	gaa	atc			816
107	Glu	Val	Asp	Ile	Met	Tyr	Gly	Glu	Gly	Ile	Ser	Lys	Glu	Gly	Glu	Ile			
108				260					265					270					
110	atc	gac	ctc	gga	aca	gag	ctt	gac	atc	gtt	caa	aag	agc	ggt	gca	tgg			864
111	Ile	Asp	Leu	Gly	Thr	Glu	Leu	Asp	Ile	Val	Gln	Lys	Ser	Gly	Ala	Trp			
112				275					280					285					
114	tac	tct	tat	cag	gag	gaa	cgc	ctt	gga	caa	ggc	cgt	gaa	aac	gcc	aaa			912
115	Tyr	Ser	Tyr	Gln	Glu	Glu	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Asn	Ala	Lys			
116				290					295				300						
118	cag	ttc	ctg	aaa	gaa	aac	aag	gat	atc	ctt	ttg	atg	att	caa	gag	cag			960
119	Gln	Phe	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Leu	Met	Ile	Gln	Glu	Gln			
120	305				310					315				320					
122	atc	cgg	gag	cac	tac	ggt	ttg	gat	act	gga	ggc	gct	gct	cct	gca	cag			1008
123	Ile	Arg	Glu	His	Tyr	Gly	Leu	Asp	Thr	Gly	Gly	Ala	Ala	Pro	Ala	Gln			
124				325						330				335					

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126 gaa gac gag gcc caa gct cag gaa gaa ctc gag ttt taa      1047
127 Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
128          340          345
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 348
133 <212> TYPE: PRT
134 <213> ORGANISM: Bacillus licheniformis DSM 13
136 <400> SEQUENCE: 2
138 Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln Ile Glu
139 1          5          10          15
142 Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu
143          20          25          30
146 Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
147          35          40          45
150 Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
151          50          55          60
154 Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu
155 65          70          75          80
158 Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala
159          85          90          95
162 Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu
163          100         105         110
166 Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu
167          115         120         125
170 Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val
171          130         135         140
174 Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser
175 145         150         155         160
178 His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu
179          165         170         175
182 Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln
183          180         185         190
186 Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro
187          195         200         205
190 Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg
191          210         215         220
194 Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr
195 225         230         235         240
198 Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala
199          245         250         255
202 Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile
203          260         265         270
206 Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp
207          275         280         285
210 Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys
211          290         295         300
214 Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln
215 305         310         315         320
218 Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln

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219                               325                               330                               335
222 Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
223                               340                               345
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 1792
228 <212> TYPE: DNA
229 <213> ORGANISM: Bacillus licheniformis
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (140)..(1336)
236 <220> FEATURE:
237 <221> NAME/KEY: gene
238 <222> LOCATION: (1)..(1792)
239 <223> OTHER INFORMATION: spoIV
242 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
244 <222> LOCATION: (140)..(142)
245 <223> OTHER INFORMATION: First codon translated as Met.
248 <400> SEQUENCE: 3
249 ggctgatgct caaacagggg cagtgcacatca ttcaaggcaa agactttgtc atcaaaacga      60
251 ttttgcctga ggaaattctg cttgaaggca cgattgagct tgtccgctat atcgattcat      120
253 aagtcggggg gaaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga      172
254                               Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly
255                               1                               5                               10
257 aag atc cag ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat      220
258 Lys Ile Gln Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn
259                               15                               20                               25
261 gaa tgc acc agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa      268
262 Glu Cys Thr Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys
263                               30                               35                               40
265 gac gcc gtc ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg      316
266 Asp Ala Val Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg
267                               45                               50                               55
269 aag gtc atc aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa      364
270 Lys Val Ile Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys
271 60                               65                               70                               75
273 ggg ttt cct ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act      412
274 Gly Phe Pro Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr
275                               80                               85                               90
277 ttt gga gtt gct gca ttt ttt atc atc atg ctc cta ttg tcc aac atg      460
278 Phe Gly Val Ala Ala Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met
279                               95                               100                               105
281 ctt tgg aaa att gat att aca gga gcc aat ccg gag aca gaa cat caa      508
282 Leu Trp Lys Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln
283                               110                               115                               120
285 atc aaa cag caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag      556
286 Ile Lys Gln Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln
287                               125                               130                               135
289 ttt tca atg ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg      604

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290 Phe Ser Met Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg
291 140                               145                               150                               155
293 gtc gaa aac atc act tgg gtg ggt att gag tta aac ggc acc gcc ctt      652
294 Val Glu Asn Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu
295                               160                               165                               170
297 cac atg aaa gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc      700
298 His Met Lys Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile
299                               175                               180                               185
301 ggt ccg agg cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa aag      748
302 Gly Pro Arg His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys
303                               190                               195                               200
305 ttc gtg gaa aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa      796
306 Phe Val Glu Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu
307                               205                               210                               215
309 aaa ggg caa atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag      844
310 Lys Gly Gln Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys
311 220                               225                               230                               235
313 caa aaa gtc gga gca aaa ggg aaa atc tac ggt gaa acc tgg tac aag      892
314 Gln Lys Val Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys
315                               240                               245                               250
317 tca aca gta acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt      940
318 Ser Thr Val Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly
319                               255                               260                               265
321 aaa gta agg aca agt cac aag cta tcc ctc gga tca ttt tcc gtg ccg      988
322 Lys Val Arg Thr Ser His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro
323                               270                               275                               280
325 atc tgg ggc ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg      1036
326 Ile Trp Gly Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr
327                               285                               290                               295
329 gag acc gaa aac ccc tcg ctg cat ttt atg aat ttt aag ctt cct gtc      1084
330 Glu Thr Glu Asn Pro Ser Leu His Phe Met Asn Phe Lys Leu Pro Val
331 300                               305                               310                               315
333 gct tat gaa aag gag cat atg agg gag agc gaa caa atc aaa agg gtg      1132
334 Ala Tyr Glu Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val
335                               320                               325                               330
337 tac tcg aaa aaa gaa gca gtt ctt gaa gga atc gaa atg gga aaa aga      1180
338 Tyr Ser Lys Lys Glu Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg
339                               335                               340                               345
341 gac atc agg aaa aaa atc ggc agc gac ggg aac att atc agt gaa aaa      1228
342 Asp Ile Arg Lys Lys Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys
343                               350                               355                               360
345 gtt ttg cac gaa acg agc gag aat ggc aaa gtt aaa ttg atc atc ctt      1276
346 Val Leu His Glu Thr Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu
347                               365                               370                               375
349 tac cag gtt att gaa gac att gtt caa aca aca cca att gtt cag gag      1324
350 Tyr Gln Val Ile Glu Asp Ile Val Gln Thr Thr Pro Ile Val Gln Glu
351 380                               385                               390                               395
353 act aaa gaa tga cagaacactt acttgcaatt catcagcaac tggaaagtcc      1376
354 Thr Lys Glu

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VERIFICATION SUMMARY

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Input Set : E:\13744- 21 US Sequence Listing.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date